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WHAT IS CLAIMED IS:

1. An isolated polynucleotide molecule comprising an operably linked transcriptional promoter, a polynucleotide sequence encoding a PIV genome or antigenome, and a transcriptional terminator, wherein said polynucleotide sequence encoding said PIV genome or antigenome is modified by introduction of a heterologous PIV sequence selected from a HPIV1 sequence, a HPIV2 sequence, a HPIV3 sequence, a BPIV sequence or a MPIV sequence to form a chimeric PIV genome or antigenome.

2. The isolated polynucleotide molecule of claim 1, wherein a gene or gene segment of human PIV3 is replaced with a counterpart gene or gene segment from a heterologous PIV.

3. The isolated polynucleotide molecule of claim 2, wherein the counterpart gene or gene segment is a HN or F glycoprotein gene or gene segment of HPIV1 or HPIV2.

4. The isolated polynucleotide molecule of claim 2, wherein an HN or F glycoprotein gene of PIV1 or PIV2 is substituted for the counterpart HN or F glycoprotein gene of HPIV3.

5. The isolated polynucleotide molecule of claim 1, wherein the polynucleotide sequence encoding the genome or antigenome incorporates a BPIV gene or gene segment.

6. The isolated polynucleotide molecule of claim 1, which incorporates a heterologous sequence from RSV.

7. The isolated polynucleotide molecule of claim 6, wherein the heterologous sequence from RSV is a G or F gene or gene segment.

8. The isolated polynucleotide molecule of claim 1, which incorporates a heterologous sequence from measles virus.

9. The isolated polynucleotide molecule of claim 8, wherein the heterologous sequence from measles virus is a HA or F gene or gene segment.

10. An isolated polynucleotide molecule comprising an operably linked transcriptional promoter, a polynucleotide sequence encoding a PIV genome or antigenome, and a transcriptional terminator, wherein said polynucleotide sequence encoding said PIV genome or antigenome is selected from the group consisting of:

i) p218(131) (SEQ ID NO: 1);

ii) p3/7(131) (SEQ ID NO: 14);

iii) p3/7(131)2G (SEQ ID NO: 15); or

iv) the isolated polynucleotide of i), ii) or iii) modified by introduction of a heterologous PIV sequence selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV sequence or a MPIV sequence or by a nucleotide insertion, rearrangement, deletion or substitution specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

11. An isolated polynucleotide molecule comprising an operably linked transcriptional promoter, a polynucleotide sequence encoding a PIV genome or antigenome, and a transcriptional terminator, wherein said polynucleotide sequence encoding said PIV genome or antigenome is modified by a nucleotide insertion, rearrangement, deletion or substitution.

12. The isolated polynucleotide molecule of claim 11, wherein said nucleotide insertion, rearrangement, deletion or substitution specifies a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation,

small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

13. The isolated polynucleotide molecule of claim 12, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates multiple *ts* mutations.

14. The isolated polynucleotide molecule of claim 12, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates multiple non-*ts* attenuating mutations.

15. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates one or more mutations of JS *cp*45.

16. The isolated polynucleotide molecule of claim 15, wherein said polynucleotide sequence encoding said PIV genome or antigenome encodes at least one amino acid substitution in the polymerase L protein.

17. The isolated polynucleotide molecule of claim 16, wherein the amino acid substitution in the polymerase L protein occurs at a position corresponding to Tyr_{942}, Leu_{992}, or Thr_{1558} of JS *cp*45.

18. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome encodes at least one amino acid substitution in the N protein.

19. The isolated polynucleotide molecule of claim 28, wherein the amino acid substitution in the N protein occurs at a position corresponding to residues Val_{96} or Ser_{389} of JS *cp*45.

20. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome encodes an amino acid substitution in the C protein.

21. The isolated polynucleotide molecule of claim 20, wherein the amino acid substitution in the C protein occurs at a position corresponding to Ile_{96} of JS *cp*45.

22. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome encodes at least one amino acid substitution in the F protein.

23. The isolated polynucleotide molecule of claim 22, wherein the amino acid substitution in the F protein occurs at a position corresponding to Ile_{420} or Ala_{450} of JS *cp*45.

24. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome encodes an amino acid substitution in the HN protein.

25. The isolated polynucleotide molecule of claim 24, wherein the amino acid substitution in the HN protein occurs at a position corresponding to residue Val_{384} of JS *cp*45.

26. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates at least one mutation in a 3' leader sequence.

27. The isolated polynucleotide molecule of claim 26, wherein the mutation in the 3' leader occurs at a position corresponding to nucleotide 23, 24, 28, or 45 of JS *cp*45.

28. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates a mutation in a N gene start sequence.

29. The isolated polynucleotide molecule of claim 28, wherein the mutation in the N gene start sequence occurs at a position corresponding to nucleotide 62 of JS *cp*45.

30. The isolated polynucleotide molecule of claim 12, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates a plurality and up to a full complement of mutations present in r*cp*45, r*cp*45 3'NCMFHN, r*cp*45 3'NL, r*cp*45 3'N, or r*cp*45 F.

31. The isolated polynucleotide molecule of claim 12, which is an antigenomic cDNA selected from r*cp*45, r*cp*45 3'NCMFHN, r*cp*45 3'NL, r*cp*45 3'N, r*cp*45 L, r*cp*45 F, r*cp*45 M, r*cp*45 HN, or r*cp*45 C.

32. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates a mutation stabilized by multiple nucleotide substitutions in a codon specifying the mutation.

33. The isolated polynucleotide molecule of claim 11, wherein said polynucleotide sequence encoding said PIV genome or antigenome incorporates a heterologous sequence from HPIV1, HPIV2, HPIV3, BPIV or MPIV to form a chimeric genome or antigenome.

34. The isolated polynucleotide molecule of claim 33, wherein said chimeric genome or antigenome incorporates one or more *ts* mutations.

35. The isolated polynucleotide molecule of claim 33, wherein said chimeric genome or antigenome incorporates one or more non-*ts* attenuating mutations.

36. The isolated polynucleotide molecule of claim 33, wherein said chimeric genome or antigenome incorporates one or more mutations of JS *cp*45.

37. The isolated polynucleotide molecule of claim 36, wherein said one or more mutations of JS *cp*45 occur in one or more PIV proteins selected from L, M, N, C, F, or HN or in a PIV extragenic sequence selected from a 3′ leader or N-gene start sequence.

38. The isolated polynucleotide molecule of claim 33, wherein said chimeric genome or antigenome incorporates multiple mutations each specifying a phenotype selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, or host range restriction.

39. The isolated polynucleotide molecule of claim 33, wherein said chimeric genome or antigenome incorporates at least one and up to a full complement of mutations present in r*cp*45, r*cp*45 3′NCMFHN, r*cp*45 3′NL, r*cp*45 3′N, or r*cp*45 F.

40. The isolated polynucleotide molecule of claim 33, wherein a mutation specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV is incorporated in a chimeric PIV background comprising a genome or antigenome having one or more PIV3 HN or F glycoprotein genes substituted by one or more counterpart PIV1 or PIV2 HN and F glycoprotein genes.

41. The isolated polynucleotide molecule of claim 33, wherein the heterologous sequence specifies a phenotypic alteration selected from attenuation, temperature-sensitivity,

cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of a chimeric PIV.

42. The isolated polynucleotide molecule of claim 11, which incorporates a cis-acting regulatory sequence of HPIV1, HPIV2, BPIV or MPIV.

43. The isolated polynucleotide molecule of claim 11, which incorporates a heterologous sequence from RSV.

44. The isolated polynucleotide molecule of claim 43, wherein the heterologous sequence from RSV is a G or F gene or gene segment.

45. The isolated polynucleotide molecule of claim 11, which incorporates a heterologous sequence from measles virus.

46. The isolated polynucleotide molecule of claim 45, wherein the heterologous sequence from measles virus is a HA or F gene or gene segment.

47. The isolated polynucleotide molecule of claim 11, which incorporates a polynucleotide sequence encoding a non-PIV molecule selected from a cytokine, a T-helper epitope, a restriction site marker, or a protein of a microbial pathogen capable of eliciting a protective immune response in a mammalian host.

48. A cell or cell-free composition including an expression vector which comprises an isolated polynucleotide molecule encoding a PIV genome or antigenome and an expression vector which comprises one or more isolated polynucleotide molecules that encode(s) N, P and L proteins of PIV, whereby expression of said PIV genome or antigenome and N, P, and L proteins yields an infectious PIV particle.

49. The cell or cell-free composition of claim 48, wherein the infectious PIV particle is a virus.

50. The cell or cell-free composition of claim 48, wherein the infectious PIV particle is a subviral particle.

51. The cell or cell-free composition of claim 48, wherein the polynucleotide encoding the PIV genome or antigenome and the one or more polynucleotides encoding N, P and L proteins of PIV are incorporated within a single vector.

52. A method for producing an infectious PIV particle from one or more isolated polynucleotide molecules encoding said PIV, comprising:

coexpressing in a cell or cell-free system an expression vector which comprises a polynucleotide molecule encoding a PIV genome or antigenome and an expression vector which comprises one or more polynucleotide molecules encoding N, P and L proteins, thereby producing an infectious PIV particle.

53. The method of claim 52, wherein the PIV genome or antigenome and the N, P, and L proteins are expressed by the same expression vector.

54. The method of claim 52, wherein the N, P, and L proteins are encoded on two or three different expression vectors.

55. The method of claim 52, wherein at least one of the N, P and L proteins is supplied by coinfection with PIV.

56. The method of claim 52, wherein the polynucleotide molecule that encodes the PIV genome or antigenome is cDNA.

57. The method of claim 52, wherein the infectious PIV particle is a virus.

58. The method of claim 52, wherein the infectious PIV particle is a subviral particle.

59. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome is a human, bovine or murine PIV sequence.

60. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome encodes the sequence of a wild-type PIV strain.

61. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome encodes HPIV3.

62. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome incorporates an attenuating mutation from a biologically derived PIV strain.

63. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome incorporates one or more *ts* mutations.

64. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome incorporates one or more non-*ts* attenuating mutations.

65. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome incorporates at least one mutation of JS *cp*45.

66. The method of claim 65, wherein the polynucleotide molecule encoding the PIV genome or antigenome incorporates multiple mutations of JS *cp*45.

67. The method of claim 65, wherein the mutation of JS *cp*45 specifies at least one amino acid substitution in the polymerase L protein.

68. The method of claim 67, wherein the amino acid substitution in the polymerase L occurs at a position corresponding to Tyr_{942}, Leu_{992}, or Thr_{1558} of JS *cp*45.

69. The method of claim 65, wherein said mutation of JS *cp*45 specifies a change in a PIV protein selected from L, M, N, C, F, or HN or in a PIV extragenic sequence selected from a 3′ leader or N gene start sequence.

70. The method of claim 52, wherein said polynucleotide molecule encoding the PIV genome or antigenome incorporates a mutation that is stabilized by multiple nucleotide substitutions in a codon which specifies the mutation.

71. The method of claim 52, wherein said polynucleotide molecule encoding said PIV genome or antigenome incorporates a plurality and up to a full complement of mutations present in *rcp*45, *rcp*45 3′NCMFHN, *rcp*45 3′NL, *rcp*45 3′N, or *rcp*45 F.

72. The method of claim 69, wherein said polynucleotide molecule encoding said PIV genome or antigenome is an antigenomic cDNA selected from *rcp*45, *rcp*45 3′NCMFHN, *rcp*45 3′NL, *rcp*45 3′N, *rcp*45 L, *rcp*45 F, *rcp*45 M, *rcp*45 HN, or *rcp*45 C.

73. The method of claim 52, wherein said polynucleotide molecule encoding said PIV genome or antigenome incorporates a heterologous sequence from HPIV1, HPIV2, HPIV3, BPIV or MPIV to form a chimeric genome or antigenome.

74. The method of claim 73, wherein the polynucleotide molecule encoding the PIV genome or antigenome

is a chimera of a HPIV3 sequence and a HPIV1, HPIV2, BPIV or MPIV sequence.

75. The method of claim 74, wherein a heterologous sequence from HPIV1 or HPIV2 encoding a gene or gene segment of an HN or F glycoprotein is substituted for a corresponding gene or gene segment of HPIV3.

76. The method of claim 73, wherein said chimeric genome or antigenome incorporates one or more *ts* mutations.

77. The method of claim 73, wherein said chimeric genome or antigenome incorporates one or more non-*ts* attenuating mutations.

78. The method of claim 73, wherein said chimeric genome or antigenome incorporates one or more mutations of JS *cp*45.

79. The method of claim 73, wherein said chimeric genome or antigenome incorporates multiple mutations each specifying a phenotype selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, or host range restriction.

80. The method of claim 73, wherein a mutation specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV is incorporated in a chimeric PIV background comprising a genome or antigenome having one or more PIV3 HN or F glycoprotein genes substituted by one or more counterpart PIV1 or PIV2 HN and F glycoprotein genes.

81. The method of claim 80, wherein one or more mutations of JS *cp*45 are incorporated in a chimeric background comprising a genome or antigenome having both PIV3 HN and F

glycoprotein genes substituted by counterpart PIV1 or PIV2 HN and F glycoprotein genes.

82. The method of claim 81, wherein said one or more mutations of JS *cp*45 occur in one or more PIV proteins selected from L, M, N, C, F, or HN or in a PIV extragenic sequence selected from a 3′ leader or N gene start sequence.

83. The method of claim 73, wherein the heterologous sequence specifies a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of a chimeric PIV.

84. The method of claim 52, wherein said polynucleotide molecule encoding said PIV genome or antigenome incorporates a heterologous sequence from RSV.

85. The method of claim 84, wherein the heterologous sequence from RSV is a G or F gene or gene segment.

86. The method of claim 52, wherein said polynucleotide molecule encoding said PIV genome or antigenome incorporates a heterologous sequence from measles virus.

87. The method of claim 86, wherein the heterologous sequence from measles virus is a HA or F gene or gene segment.

88. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome is selected from:

i) p218(131) (SEQ ID NO: 1);

ii) p3/7(131) (SEQ ID NO: 14);

iii) p3/7(131)2G (SEQ ID NO: 15); or

iv) the polynucleotide molecule of i), ii) or iii) modified by introduction of a heterologous PIV sequence

selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV sequence or a MPIV sequence or by a nucleotide insertion, rearrangement, deletion or substitution specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

89. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome is selected from:

i) p218(131) (SEQ ID NO: 1);

ii) p3/7(131) (SEQ ID NO: 14);

iii) p3/7(131)2G (SEQ ID NO: 15); or

iv) the polynucleotide molecule of i), ii) or iii) modified by introduction of a heterologous PIV sequence selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV sequence or a MPIV sequence and by a nucleotide insertion, rearrangement, deletion or substitution different from said introduction of said heterologous PIV sequence specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

90. The method of claim 52, wherein the polynucleotide molecule encoding the PIV genome or antigenome is modified to encode a non-PIV molecule selected from a cytokine, a T-helper epitope, a restriction site marker, or a protein of a microbial pathogen capable of eliciting a protective immune response in a mammalian host.

91. An isolated infectious PIV particle which comprises a recombinant PIV genome or antigenome, a N protein, a P protein, and a L protein.

92. The isolated infectious PIV particle of claim 91, which is a subviral particle.

93. The isolated infectious PIV particle of claim 91, which is a virus.

94. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome incorporates a heterologous sequence from RSV or measles virus.

95. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome is a cDNA.

96. The isolated infectious PIV particle of claim 91, which is a human PIV.

97. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome is a chimera of heterologous PIV sequences selected from HPIV1, HPIV2, HPIV3, BPIV, or MPIV sequences.

98. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome is selected from:

i) p218(131) (SEQ ID NO: 1);

ii) p3/7(131) (SEQ ID NO: 14);

iii) p3/7(131)2G (SEQ ID NO: 15); or

iv) the genome or antigenome of i), ii) or iii) modified by introduction of a heterologous PIV sequence selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV sequence or a MPIV sequence or by a nucleotide insertion, rearrangement, deletion or substitution specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

99. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome is selected from:

i) p218(131) (SEQ ID NO: 1);

ii) p3/7(131) (SEQ ID NO: 14);

iii) p3/7(131)2G (SEQ ID NO: 15); or

iv) the genome or antigenome of i), ii) or iii) modified by introduction of a heterologous PIV sequence selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV sequence or a MPIV sequence and by a nucleotide insertion, rearrangement, deletion or substitution different from said introduction of said heterologous PIV sequence specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

100. The isolated infectious PIV particle of claim 91, wherein the counterpart gene or gene segment is a gene or gene segment of the HN or F glycoprotein gene of HPIV1 or HPIV2.

101. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome incorporates a heterologous sequence from RSV or measles virus.

102. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome is modified by a nucleotide insertion, rearrangement, deletion or substitution encoding a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

103. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome incorporates multiple *ts* mutations.

104. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome incorporates multiple non-*ts* attenuating mutations.

105. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome incorporates at least one mutation of JS *cp*45.

106. The isolated infectious PIV particle of claim 105, wherein the mutation of JS *cp*45 specifies an amino acid substitution in the polymerase L protein.

107. The isolated infectious PIV particle of claim 97, wherein said chimeric genome or antigenome incorporates one or more *ts* mutations.

108. The isolated infectious PIV particle of claim 97, wherein said chimeric genome or antigenome incorporates one or more non-*ts* attenuating mutations.

109. The isolated infectious PIV particle of claim 97, wherein said chimeric genome or antigenome incorporates one or more mutations of JS *cp*45.

110. The isolated infectious PIV particle of claim 129, wherein said chimeric genome or antigenome incorporates multiple mutations each specifying a phenotype selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, or host range restriction.

111. The isolated infectious PIV particle of claim 109, wherein said chimeric genome or antigenome incorporates at least one and up to a full complement of mutations present in r*cp*45, r*cp*45 3'NCMFHN, r*cp*45 3'NL, r*cp*45 3'N, or r*cp*45 F.

112. The isolated infectious PIV particle of claim 91, wherein a mutation specifying a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV is incorporated in a chimeric PIV background comprising a genome or antigenome having one or more PIV3 HN or F glycoprotein genes or gene

segments substituted by one or more counterpart PIV1 or PIV2 HN and F glycoprotein genes or gene segments.

113. The isolated infectious PIV particle of claim 112, wherein one or more mutations of JS *cp*45 are incorporated in said chimeric background.

114. The isolated infectious PIV particle of claim of claim 113, wherein said one or more mutations of JS *cp*45 occur in one or more PIV proteins selected from L, M, N, C, F, or HN or in a PIV extragenic sequence selected from a 3' leader or N gene start sequence.

115. The isolated infectious PIV particle of claim 91, wherein the recombinant PIV genome or antigenome is modified to encode a non-PIV molecule selected from a cytokine, a T-helper epitope, a restriction site marker, or a protein of a microbial pathogen capable of eliciting a protective immune response in a mammalian host.

116. The isolated infectious PIV particle of claim 91, further comprising an RSV antigen or epitope which elicits protective immunity to RSV in an immunized host.

117. The isolated infectious PIV particle of claim 91, which is selected from r942, r992, r1558, r942/992, r992/1558, r942/1558, or r942/992/1558, r*cp*45 3´N, r*cp*45 C, r*cp*45 M, r*cp*45 F, r*cp*45 HN, r*cp*45L, r*cp*45 3´NL, r*cp*45 3´NCMFHN, and r*cp*45.

118. An immunogenic composition comprising an immunogenically effective amount of an infectious PIV particle in a pharmaceutically acceptable carrier, said PIV particle comprising a recombinant PIV genome or antigenome, a N protein, a P protein, and a L protein.

119. The immunogenic composition of claim 118, wherein said infectious PIV particle is a subviral particle.

120. The immunogenic composition of claim 118, wherein said infectious PIV particle is a virus.

121. The immunogenic composition of claim 118, wherein the recombinant PIV genome or antigenome incorporates a heterologous sequence from RSV or measles virus.

122. The immunogenic composition of claim 118, wherein the recombinant PIV genome or antigenome is a chimera of heterologous PIV sequences selected from HPIV1, HPIV2, HPIV3, BPIV, or MPIV sequences to form an infectious, chimeric PIV particle.

123. The immunogenic composition of claim 118, wherein the recombinant PIV genome or antigenome encodes a human PIV in which a gene or gene segment is replaced with a counterpart gene or gene segment from a heterologous PIV.

124. The immunogenic composition of claim 123, wherein one or both HN and F glycoprotein genes of HPIV1 are substituted for HN and F glycoprotein genes of HPIV3 to form said infectious, chimeric PIV particle.

125. The immunogenic composition of claim 123, wherein the recombinant PIV genome or antigenome of said infectious, chimeric PIV particle is modified by a nucleotide insertion, rearrangement, deletion or substitution encoding a phenotypic alteration selected from attenuation, temperature-sensitivity, cold-adaptation, small plaque size, host range restriction, or a change in an immunogenic epitope of PIV.

126. The immunogenic composition of claim 125, wherein said recombinant PIV genome or antigenome incorporates multiple mutations selected from *ts* and non-*ts* attenuating mutations to form an attenuated, infectious, chimeric PIV particle.

127. The immunogenic composition of claim 118, wherein the recombinant PIV genome or antigenome incorporates a mutation of JS *cp*45.

128. The immunogenic composition of claim 118, wherein the recombinant PIV genome or antigenome incorporates multiple mutations of JS *cp*45.